

1/24

3/24
X

2/24	3/24
4/24	5/24
6/24	7/24

2/24

- 60 tgaaaagatagaataaatggcctcg
1 ATGGCCGCCGCCAGCCCTGCTGGCCGAC
1 M A R P A L L G E
61 GGCCAAGTTGCCCGGCCACAGAAGTT
211 G Q V A A A T E V
121 GAAAATCTCTGCACGATAATATGGACG
41 E N L C T I I W T
181 ACTCTCAGATATTAGTCACTTTGAT
61 T L R Y F S H F D
241 CATCGTAAAGAGGAATTACCCCTGGAT
81 H R K E E L P L D
301 AGTCGCAATGAAAGTCAGAACGCCTAGC
101 S A N E S E K P S
361 GGTGATCCTGACTCCGCTGTGACTGAG
121 G D P E S A V T E
421 AACGTCGTCCTGCCTTCCTGGAAAGGAAT

Fig. 1(i)

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ccggaaatttccggcaacgagcccgaggcgaggccctgc

C^TGTTGGTGCTGCTACT^TGTCGACCGCCACCGTG
L L V I L L W T A T V

CAGCCACCTGTGACGAA^TTGAGCGTCTCTGTQ
Q I P P V T H I S V S V

TGGAGTCCTCCTGAACGAGCCACTCCA^AATTGC
W S P P E G A S P H C

GACCAACACGGATAAGAAAATTGCTCCAGA^AACT
D Q Q D K K I A P E T

GAGAAAATCTGTCTGCCAGGTGGGCTCTCAGTGT
E K I C L Q V G S Q C

CCTTTGGTGA^{AAA}ACTGCATCTCACCCCCCTGAA
P L V K K C I S | P P E

C^TCAACTGCAT^TTGGCATAACCTCAGCTATATG
I K C I W H N L S Y M

ACAAGCCCTGACACACACTATACTCTGTACTAT

Fig. 1(ii)

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481	TGGTACAGCACCCCTGGACAAAAGTCGT
161	W Y S S L E K S R
541	ATPGCTPGTCCCTTTAAATTGACTAAA
181	I A C S F K L T K
601	ATAATGGTCAAGGATAATGCTGGGAA ¹¹
261	I M V K D N A G K
661	TCCTATG TGAAACCTGATCCTCCACAT
221	S Y V K P D P P H
721	TTAGTGCAGTGGAAGAATCCACAAAAT
241	L V Q W K N P Q N
781	GTCAATAATACTCAAACCGACCGACAT
261	V N N T Q T D R H
841	AATTCCTCCAAATCTGATAGAAACATGGAG
281	N S E S D R N M E
901	GCGCACCCCTGTCATACACAGTCAGACTA
301	A D A V Y T V R V

Fig. 1(iii)

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CAATGTGAAAACATCTATAGAGAACGTCAACAC
Q C E N T Y R E G Q H

GTCGAACCTAGTTTCAACATCAGAACGTCAA
V E P S F E H Q N V Q

ATPAGGCCATCCCGCAAAATACTGTCCTTTAACT
T R P S C K T V S L T

ATTAACATCTCTCCTCAAAAATGGTGCCTTA
T K H L L L K N G A L

TTTAGAAGCAGATGCTTAACCTATGAAGTGGAG
F R S R C L T Y E V E

AATATTTAGAGGTGAAAGAGGACAAATGCCAG
N I L E V E E D K C Q

GGTACAAGTTGTTCCAACCTCCCTGGTGTCTT
G T S C F Q L P G V L

ACACTCAAAACAAACAACTTATGCTTGTGAC
R V K T N K L C F D D

Fig. 1(IV)

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1021	TTCTACACCACCATGTTACTCACCATT
341	F Y T T M L L T I
1081	CTPTTPIPACCTPGAAAAGGCCTPAAGATC
361	L F Y L K R L K I
1141	ATT'TTTAAAGAAATGTTGGAGACCAG
381	I F K E M F G D Q
1201	ATCTATGAGAAACAAATCCAAAGAAGAA
401	I Y E K Q S K E E
1261	AAACCAAGCTCCTTGA
421	tggggagaagtg K A A P *
1321	gatttattgeatttcattttgttatac
1381	cTTaaaaaacaggcagcttcataagagc
1441	ccaaacccaaaggagcttcattccaaga
1501	ccctaaaagcagatgtttgccaaatac
1561	accatcaattcataatcaggaattg

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CCAGTCTTTGTCGGAGTGGCACTCATAAATCCTC
P V F V A V A V I I L

AATTATAATTCTCCAATTCCTGATCCTGGCAAAG
T I F P P I P D P G K

AATGATGATAACCCTGCAC TGGAAGAACTATGAC
H D D T L H W K K Y D

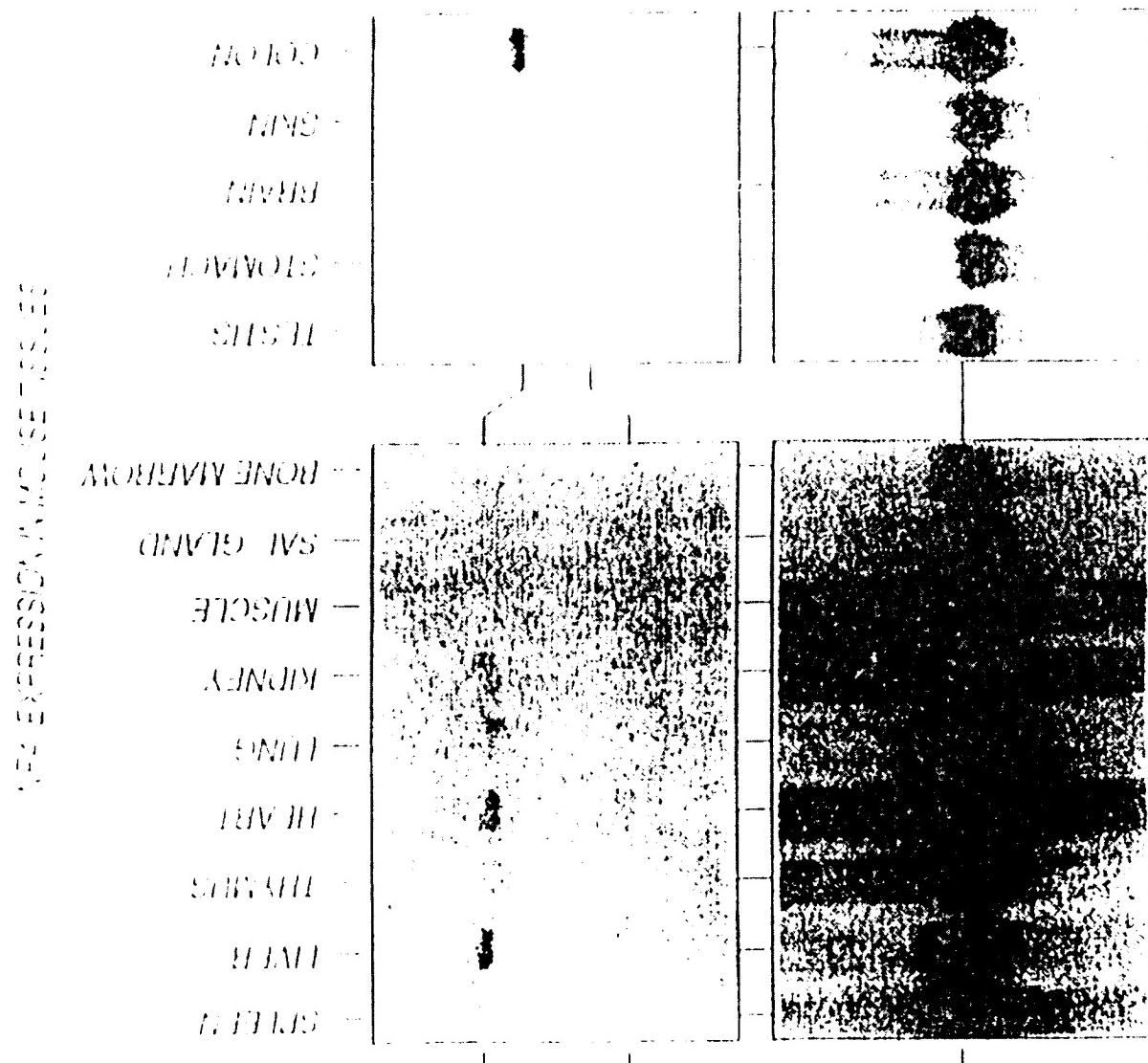
ACCGAATTCTGTAGTGCTCATAGAAAACCTGAAG
T D S V V L I E N L K

atttcttttttgttcaatgtgacccctgtgaa

tgggggacttgttaaataaaaaactgaaaactact
cacagggttttgttgacttttgtcatgtgaaaac
aaagcaagagtttttgttcaatgttggatgttcaat
cccaaacttagaggacaaagacaaggggacaatgt
tgtatgttgttcaatgttcaatgttcaatgttcaatgt

5'->3'

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Fig

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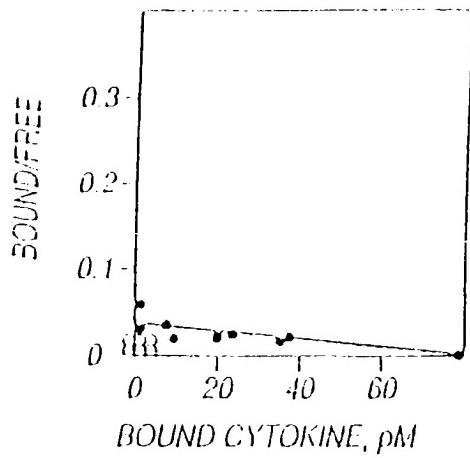


Fig. 3(A)

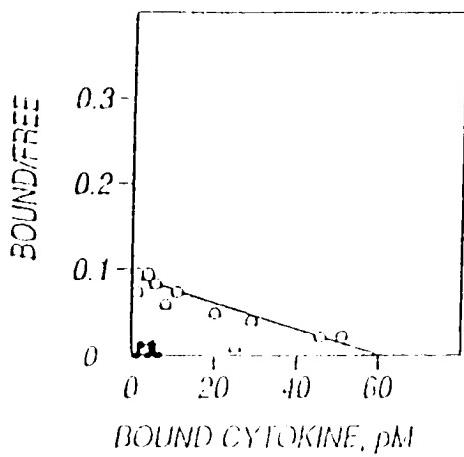


Fig. 3(B)

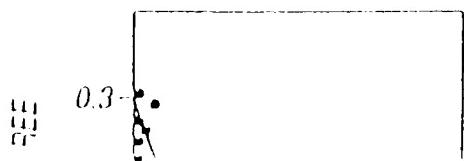


Fig. 3(C)

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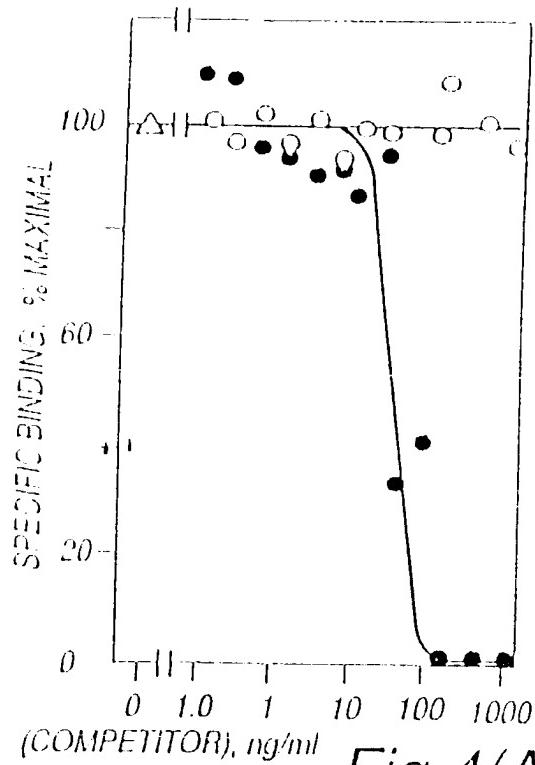


Fig. 4(A)

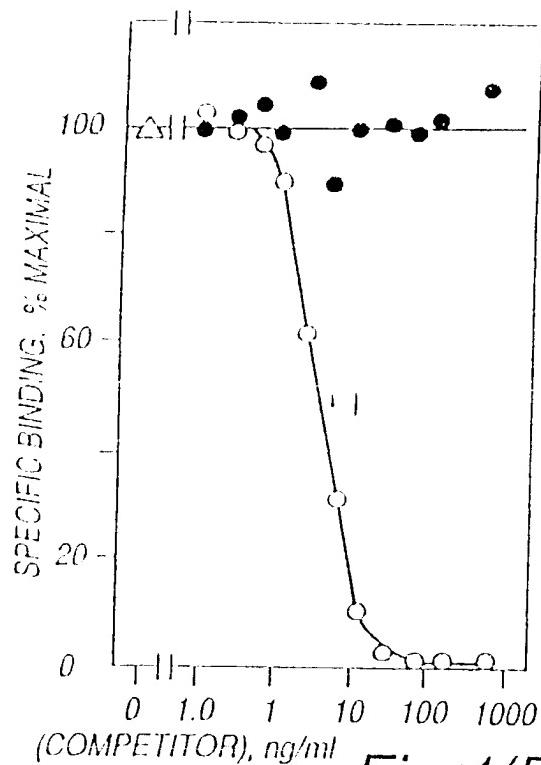
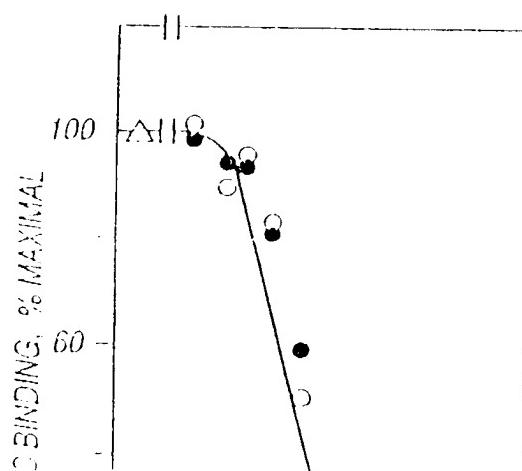
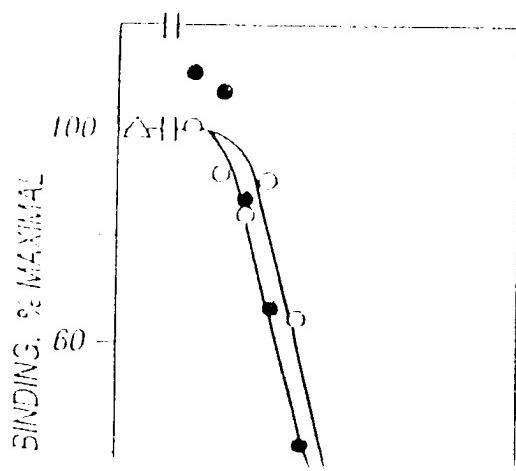


Fig. 4(B)



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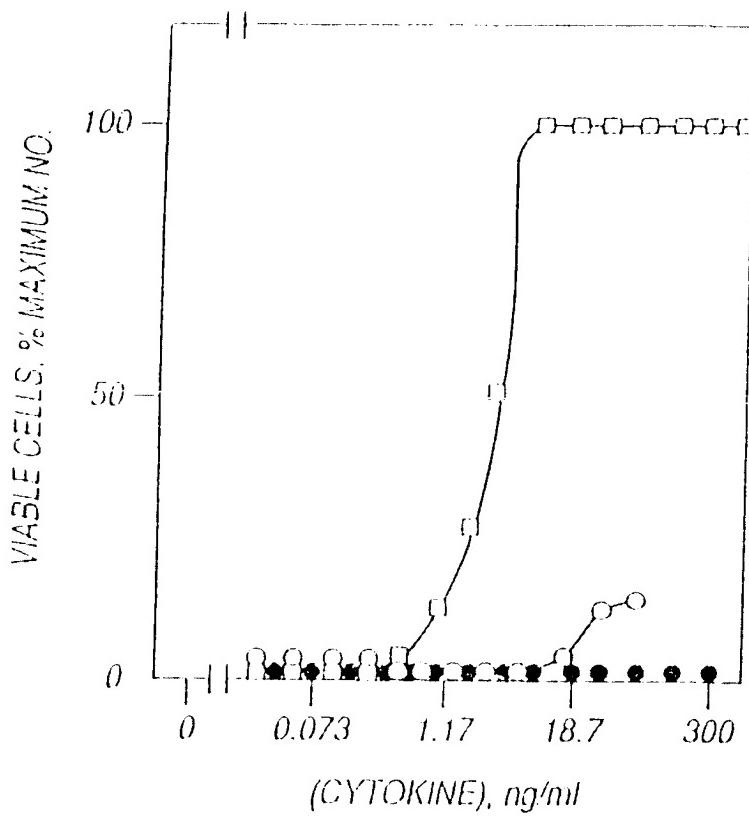
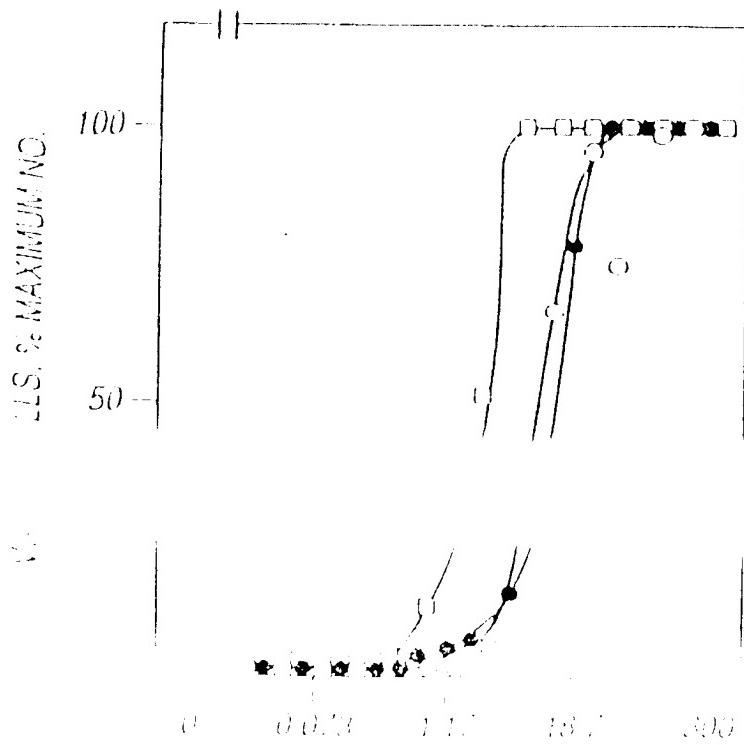


Fig. 5(A)



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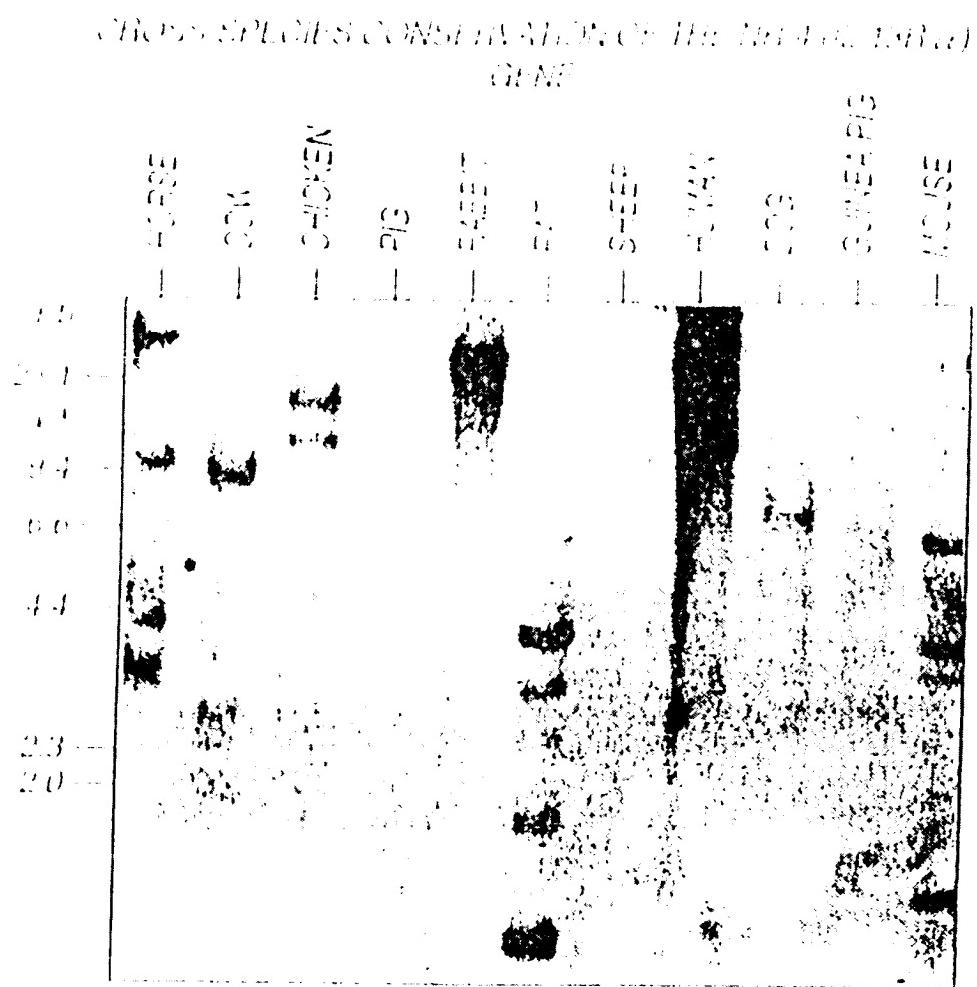


Fig. 6

(Fig. 6)

CHROMATOPHORES CONCENTRATED IN MUSCLE TISSUE

(Fig. 6)

CHROMATOPHORES CONCENTRATED IN MUSCLE TISSUE

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16/24	17/24
18/24	19/24
20/24	21/24

Fig. 7

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H	gag t c t a a c a c g g a c c a a g g a g t t a a c					
M	- 60	t g a a a a g a t a g a a t a a a t g g c c t c g t g c				
H	M E W P A R I C G					
	ATGGAGTGGCCCCCGGGCTCTGGCGGGC					
*	*	*	*	*	II	
M	11	ATGGCCGGCCAGGGCTCCTGGCGAGC				
M	1	M A R P A L L G E				
H	G G G G A P T E T					
H	GGGGGCCGGCCGGCCACTACGGAAACTC					
*	*	*	*	*		
M	61	GGCCAAGTTGCCGGCCACAGAAGTTG				
M	21	G Q V A A A T E V				
H	E N L C T V I W T					
H	GAAAACCTCTGCACAGTAATATGGACAT					
*	*	*	*	*	*	*
M	121	GAAAATCTCTCCACGATAATATGGACGT				
H	E N L C T T I W T					
H	S L W Y F S H F G					
H	AGTCTATGGTATTTAGTCATTGCG					
*	*	*	*	*	*	
M	181	ACTCTCAGATAATTTAGTCACPTTGATG				

Fig. 7(i)

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a c g t g e g g c c g g g t t c c g a g g c g a g a g g c t g c
c g a a t t c g g c a c g a g c c g a g g c g a g g c c t g c

L W A L L I C A G G G G
TGTGGGCCCTGCTGCTCTGGCCCCGGGGGGGG.
* * * * * * * * * * *
TGTGGTGCTCCTACTCTGGACCGCCACCGTC - -
L L V L L L W T A T V -

Q P P V T N L S V S V
AGCCACCTGTGACAAATTGAGTGTCTCTGTT
* * * * * * * * * * *
AGCCACCTGTGACGAATTGAGCCTCTCTGTC
Q P P V T N L S V S V

W N P P E G A S S N C
CGAATCCACCCGAGGGAGCCACCTCAAATTGT
* * * * * * * * * *
CGACTCCTCCTGAAAGGACCCAGTCCTAAATTGC
W S P P E G A S P N C

D K Q D K K I A P E T
ACAAACAGATAAGAAAATAGCTCCGGAAACT
* * * * * * * * * *
ACCAACAGATAACAATAGCTCCAGAAACT

Fig. 7(ii)

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H	R	R	S	I	E	V	P	L	N
H	CGTCGTTCAATAGAACTACCCCTGAATG	*		*	*	*	*		
M 241	CATCGTAAACAGGAATTACCCCTGGATG								
M 81	H R K E E L P L D								
H 11	S T N E S E K P S								
H	AGCACCAATGAGAGTGAGAAGCCTAGCA	*	*	*	*	*	*	*	*
M 301	ACTGCCAATGAAAGTGAGAAGCCTAGCC								
M 101	S A N E S E K P S								
H	G D P E S A V T E								
H	GGTGATCCTGACTCTGCTGTGACTGAAAC	*	*	*	*	*	*	*	*
M 361	GGTGATCCTGAGTCCGCTGTGACTGAGC								
M 121	G D P E S A V T E								
H	K C S W L P G R N								
H	AAGTGTTCCTGGCTCCCTGCAAGGAATA	*	*	*	*	*	*	*	*
M 421	AAGTGTTCCTGGCTCCCTGCAAGGAATA								
M 141	K C S W L P G R N								
H	W H R S L E K I H								
H	GGTGATCCTGAGTCCGCTGTGACTGAGC								

Fig. 7(iii)

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E	R	I	C	L	Q	V	G	S	Q	C
AGAGGATTTGTCTGC	AAGTGGGGTCCCAGTGT	*	*	*	*	*	*	*	*	*
AGAAAATCTG	TCTGCAGCTGGGCTCTCA	G	TGT							
E	K	I	C	L	Q	V	G	S	Q	C
T	L	V	E	K	C	I	S	P	P	E
TTTTGGTTGAA	AAAATGCATCTCACCCCCAGAA	*	*	*	*	*	*	*	*	*
CTTTGGTGAA	AAACTGCATCTCACCCCCCTGAA									
P	L	V	K	K	C	I	S	P	P	E
L	Q	C	I	W	H	N	L	S	Y	M
TTCAATGCATTG	CCACAAACCTGAGCTACATG	*	*	*	*	*	*	*	*	*
TC	AAAGTGCA	TTTGCCATAACCTGAGCTATATG								
L	K	C	I	W	H	N	L	S	Y	M
T	S	P	D	T	H	Y	T	L	Y	Y
CCAGTCCC	GACACTAAC	TAT	ACTPACTCTACTAT	*	*	*	*	*	*	*
CAAGCCCTGACACAC	ACTATACTCTG	TA	CTACTAT							
T	S	P	D	T	H	Y	T	L	Y	Y
T	S	P	D	T	H	Y	T	C	O	Y

Fig. 7(iv)

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		*		*	*	*	*	
M	481	TGGTACACCAGCCTGGAGAAAAGTCGTC						
M	161	W Y S S L E K S R						
H		F G C S F D L T K						
H		TTTGGCTTGTTCCTTTGATCTGACCAAAAG		*	*	*	*	*
M	541	ATTGCTTGTTCCTTTAAATTGACTAAAG						
M	181	T A C S F K L T K						
H		Q I M V K D N A G						
H		CAAATAATGGTCAAGGATAATGCAGGAA	*	*	*	*	*	*
M	601	CAAATAATGGTCAAGGATAATGCTGGGA						
M	201	Q I M V K D N A G						
H		T S R V K P D P P						
H		ACTTCCCCGTGTGAAACCTGATCCTCCAC	*	*	*	*	*	*
M	661	ACTTCCTATGTGAAACCTGATCCTCCAC						
M	221	T S Y V K P D P P						
H		L Y V Q W E N P Q						
H		CTATATGTGCAATGGAGAATCCACAGA	*	*	*	*	*	*
M	721	TTATTPAGTCCAGTCGAACAATCCACAAA						
M	511	TTATTPAGTCCAGTCGAACAATCCACAAA						

Fig. 7(v)

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Fig. 7(vi)

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H		E	V	N	N	S	Q	T	E	T
H		GAAGTCAATAACAGCCAAACTGAGACAC								
		*	*	*	*	*	*	*		
M	781	GAGGTCAATAATACTCAAACCGACCGAC								
M	261	E	V	N	N	T	Q	T	D	R
H		E	N	P	E	F	E	R	N	V
H		GAGAATCCAGAATTGTGAGAGAAATGTGG								
		*	*	*				*	*	
M	841	CAGAATTCCGAATCTGATAGAACATGG								
M	281	Q	N	S	E	S	D	R	N	M
H		L	P	D	T	L	N	T	V	R
H		CTTCCTGATACTTTGAACACAGTCAGAA								
		*	*	*			*	*	*	
M	901	CTTGCCGACCGCTGTCTACACAGTCAGAG								
M	301	L	A	D	A	V	Y	T	V	R
H		D	D	K	L	W	S	N	W	S
H		GATGACAAACTCTGGACTGATTGGAGTG								
		*	*	*	*	*	*	*	*	*
M	961	GACAACAAACTCTGGACTGATTGGAGTG								
M	321	D	N	K	L	W	S	D	W	S
H		W	I	V	I	W	R	R	R	R

Fig. 7(vii)

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H	N	V	F	Y	V	Q	E	A	K	C
A	T	A	A	G	T	T	T	C	A	G
*	*	*	*	*	*	*	*	*	*	*
A	T	A	A	T	T	T	A	G	A	C
H	N	I	L	E	V	E	E	D	K	C
*	*	*	*	*	*	*	*	*	*	*
E	N	T	S	C	F	M	V	P	G	V
A	G	A	A	T	A	C	T	G	T	T
*	*	*	*	*	*	*	*	*	*	*
A	G	G	T	A	C	A	G	T	T	C
A	G	G	T	A	C	A	C	T	C	T
A	G	G	T	A	C	A	C	T	C	T
H	G	T	S	C	F	Q	L	P	G	V
*	*	*	*	*	*	*	*	*	*	*
I	R	V	K	T	N	K	L	C	Y	E
T	A	A	G	A	T	C	A	T	G	G
*	*	*	*	*	*	*	*	*	*	*
T	A	A	G	A	T	C	A	T	G	T
V	R	V	K	T	N	K	L	C	F	D
*	*	*	*	*	*	*	*	*	*	*
Q	E	M	S	I	G	K	K	R	N	S
A	A	G	A	A	T	G	A	T	G	T
*	*	*	*	*	*	*	*	*	*	*
A	A	G	C	A	C	T	A	G	G	C
A	A	G	C	A	C	T	A	G	G	C
A	A	G	C	A	C	T	A	G	G	C
E	A	Q	S	I	G	K	E	Q	N	S
*	*	*	*	*	*	*	*	*	*	*
V	P	V	T	V	A	G	A	T	T	V

Fig. 7(viii)

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		*	*	*	*	*	*	*
M	1021	ACCTTCTACACCACCATGTTACTCACCA						
M	341	T F Y T T M L L T						
H		L L L Y L K R L K						
H		CTCCCTGCTTTACCTAAAAAGGCTCAAGA						
M	1081	CTCCCTTTTACCTPGAAAAGGCTTAAGA						
M	361	L L F Y L K R L K						
H		K I F K E M F G D						
H		AAGATTTAAAGAAATGTTGGAGACC						
M	1141	AAGATTTAAAGAAATGTTGGAGACC						
M	381	K I F K E M F G D						
H		D I Y E K Q T K E						
H		GACATCTATGAGAACCAAACCAAGGAGG						
M	1201	GACATCTATGAGAACCAAACCAAGGAGG						
M	401	D I Y E K Q S K E						
H		K K A S Q *						
H		AAGAAAGCCTCTCAGTPGAtggagataat						
M	1261	AAGAAAGCAGCTCCTPGAtggggagaag						
H	101	V K N D *						

Fig. 7(ix)

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* * * * * * *
 TTCCAGTCTTGTGTCGCAGTGGCAGTCATAATC
 I P V F V A V A V I I
 I I I F P P I P D P G
 TTATTTATATTCCCTCCAATTCCCTGATCCTGGC
 * * * * * * * * * * * * *
 TCAATTATATTCCCTCCAATTCCCTGATCCTGGC
 I I I F P P I P D P G
 Q N D D T L H W K K Y
 AGAATGATGATACTCTGCAC TGGAAGAAAGTAC
 * * * * * * * * * * * *
 AGAATGATGATAACCCTGCAC TGGAAGAAAGTAT
 Q N D D T L H W K K Y
 E T D S V V L I E N L
 AAACCGACTCTGTACTGCTGATAGAAAACCTG
 * * * * * * * * * * * *
 AAACCGATTCTGTACTGCTGATAGAAAACCTG
 E T D S V V L I E N L
 ttatTTttacTTcaCTgtgacCTtgagaaga
 tqaTTtttTtttqacTTcaatgtgaccctgt

Fig. 7(x)

24.24

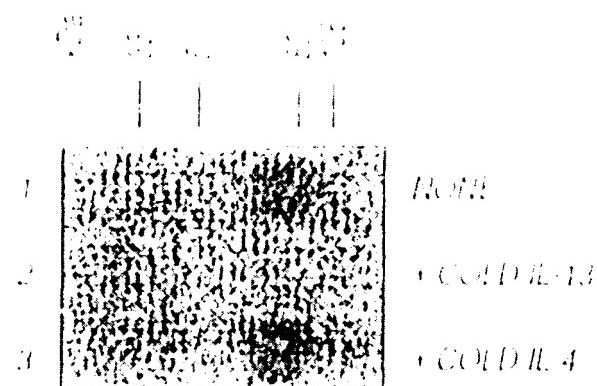


Fig. 8



Fig. 9